



CDS: SPAC4F10.02



WARNING: 30th July 2008

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General Information

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Systematic Name SPAC4F10.02
 Status role inferred from homology
 Product aminopeptidase (predicted)
 Type CDS
 Sequence DNA and Protein

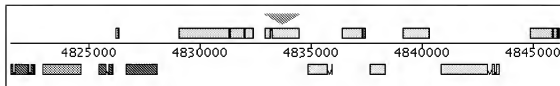
Location

Chromosome I
 Contig Location 4832929..4834428 (Unspliced length: 1500 bp)
 Exons join(4832929..4833160 , 4833257..4834428) (Spliced length: 1404 bp)

[Region download
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Artemis\)](#)

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Context Map:



hus1 SPAC20G4.05c adf1 SPAC20G4.09 sts1 SPAC20G4.08 >SPAC4F10.02< SPAC4F10.03c SPAC4F10.04
 SPAC4F10.05c SPAC4F10.06 atg13 mug126

Curation

Term
 conserved eukaryotic family
 metallopeptidase
 peptidase family M18
 similar to *S. cerevisiae* YHR113W

Other genes annotated to this term
 (866 Others)
 (7 Others)
 (0 Others)
 (0 Others)

Predicted Peptide Properties

| | | | |
|-----------------------|-----------|-------------|------|
| Mass | 51.7 kDa | Amino acids | 467 |
| Isoelectric point | pH 5.7 | Charge | -6.0 |
| Signal Peptide | Not found | | |
| Transmembrane Domains | 0 found | | |
| GPI Anchor | Not found | | |

Gene Ontology Annotation

| Term (browse Amigo) | Qualifier Evidence | Other genes annotated to this term |
|--|---|------------------------------------|
| Biological Process | | |
| proteolysis | ISS (PMID:17072883) with Pfam:PF02127 | 228 others |
| Cellular Component | | |
| cytoplasm | ISS (PMID:17072883) with SGD:S000001155 | 4204 others |
| cytosol | IDA (PMID:16823372) | 2322 others |
| fungal-type vacuole | ISS (PMID:17072883) with Pfam:PF02127 | 30 others |
| Molecular Function | | |
| aspartyl aminopeptidase activity | ISS (PMID:17072883) with SGD:S000001155 | none |
| metallopeptidase activity | IEA (GOA:spkw GO_REF:0000004) with SP_KW:KW-0482 | 39 others |
| zinc ion binding | IEA (GOA:interpro GO_REF:0000002) with InterPro:IPR001948 | 353 others |

Catalytic Activity

EC 3.4.11.- : IUBMB

Published Expression Profiles

Gene Expression Viewer [Cell Cycle](#) [Meiosis](#) [Environmental Stress](#) [Pheromone Response/Mating](#)
 TranscriptomeViewer SPAC4F10.02 High-resolution view of transcripts in neighbourhood

Literature

Search for in PubMed

Domain Information

[View Pfam domain structure for this gene product](#)[View SCOP superfamily](#)

| DB | Accs | Description |
|----------|---------------------------|---|
| Pfam | PF02127 | Aminopeptidase I zinc metalloprotease (M18) |
| MEROPS | M18.002 | MEROPS |
| InterPro | IPR001948 | Peptidase M18, aminopeptidase I |
| PRINTS | PR00932 | Aminopeptidase I zinc metalloprotease (M18) signature |

Database Cross-References

| DB | Accs | Description |
|------------------|-----------------------------|---|
| UniProtKB | Q36014 | Putative aspartyl aminopeptidase (EC 3.4.11.21). |
| EMBL | CU329670 | Schizosaccharomyces pombe chromosome I |
| EMBL | D89276 | Schizosaccharomyces pombe mRNA, partial cds, clone: SY 1794. |
| Biotwiki | SPAC4F10.02 | Biotwiki |
| NCBI Entrez Gene | SPAC4F10.02 | NCBI Entrez Gene |
| FYSSION | SPAC4F10.02 | FYSSION |
| GermOnline | SPAC4F10.02 | GermOnline |
| NBRP | SPAC4F10.02 | Fission yeast strain database, National BioResource Project (Japan) |
| PIR | T38806 | PIR |

PIR [T43206](#) PIR
YOGY [SPAC4F10.02](#) Retrieval of eukaryotic orthologs

UniProtKB Annotation For This Protein

| | |
|----------------------|---|
| Catalytic Activity | Release of an N-terminal aspartate or glutamate from a peptide, with a preference for aspartate. |
| Cofactor | Binds 1 zinc ion per subunit (By similarity). |
| Similarity | Belongs to the peptidase M18 family. |
| Subcellular Location | Cytoplasm (By similarity). |
| Keywords | Aminopeptidase (10 others), Complete proteome (4982 others), Cytoplasm (861 others), Hydrolase (451 others), Metal-binding (451 others), Metalloprotease (21 others), Protease (90 others), Zinc (302 others) |

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